DC
#12

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Revised 01/29/2002

PCT89
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        RAW SEQUENCE LISTING              DATE: 10/24/2002
        PATENT APPLICATION:  US/10/019,980A     TIME: 16:07:59

        Input Set : A:\EP.txt
        Output Set: N:\CRF4\10242002\J019980A.raw

  3 <110> APPLICANT: Berthelsen, Jens
  4        Toma, Salvatore
  5        Isacchi, Antonella
  7 <120> TITLE OF INVENTION: Tankyrase Homolog Protein (THP), Nucleic Acids, And Methods
  8        Related To The Same
 10 <130> FILE REFERENCE: PHRM0373
 12 <140> CURRENT APPLICATION NUMBER: 10/019,980A
 13 <141> CURRENT FILING DATE: 1999-07-03
 15 <150> PRIOR APPLICATION NUMBER: 09/350,982
 16 <151> PRIOR FILING DATE: 1999-07-09
 18 <150> PRIOR APPLICATION NUMBER: PCT/EP00/06609
 19 <151> PRIOR FILING DATE: 2000-07-03
 21 <160> NUMBER OF SEQ ID NOS: 10
 23 <170> SOFTWARE: PatentIn version 3.1
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C--> 13 on line shown above

ERRORED SEQUENCES

Wrapped nucleics throughout.
See error summary sheet item 1.

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 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 20
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: PCR Primers
 33 <400> SEQUENCE: 1
 34 gagtatttgt tacaacacgg
 35 20
 38 <210> SEQ ID NO: 2
 39 <211> LENGTH: 18
 40 <212> TYPE: DNA
 41 <213> ORGANISM: Artificial Sequence
 43 <220> FEATURE:
 44 <223> OTHER INFORMATION: PCR Primers
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 47 aatctccttc agctcctt
 48 18
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 53 <212> TYPE: DNA
 54 <213> ORGANISM: Homo sapiens
 56 <220> FEATURE:
 57 <221> NAME/KEY: misc_feature
 58 <222> LOCATION: (1124)..(1124)
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E--> 34 gagtatttgt tacaacacgg

E--> 47 aatctccttc agctcctt

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E--> 72 cgcgagcgcc gcggccgagg ccgtggagcc ggccgcccga gagctgttcg aggcgtgccg
    73 120
E--> 75 caacggggac gtggaacgag tcaagaggct ggtgacgcct gagaaggtga acagccgcga
    76 180
E--> 78 cacggcgggc aggaaatcca ccccgctgca cctcgccgca ggttttgggc ggaaagacgt
    79 240
E--> 81 agttgaatat ttgcttcaga atggtgcaaa tgtccaagca cgtgatgatg ggggccttat
    82 300
E--> 84 tcctcttcat aatgcatgct cttttggtca tgctgaagta gtcaatctcc ttttgcgaca
    85 360
E--> 87 tggtgcagac cccaatgctc gagataattg gaattatact cctctccatg aagctgcaat
    88 420
E--> 90 taaaggaaag attgatgttt gcattgtgct gttacagcat ggagctgagc caaccatccg
    91 480
E--> 93 aaatacagat ggaaggacag cattggattt agcagatcca tctgccaaag cagtgcttac
    94 540
E--> 96 tggtgaatat aagaaagatg aactcttaga aagtgccagg agtggcaatg aagaaaaat
    97 600
E--> 99 gatggctcta ctcacaccat taaatgtcaa ctgccacgca agtgatggca gaaagtcaac
   100 660
E--> 102 tccattacat ttggcagcag gatataacag agtaaagatt gtacagctgt tactgcaaca
   103 720
E--> 105 tggagctgat gtccatgcta aagataaagg tgatctggta ccattacaca atgcctgttc
   106 780
E--> 108 ttatggtcat tatgaagtaa ctgaactttt ggtcaagcat ggtgcctgtg taaatgcaat
   109 840
E--> 111 ggacttgtgg caattcactc ctcttcatga ggcagcttct aagaacaggg ttgaagtatg
   112 900
E--> 114 ttctcttctc ttaagttatg gtgcagaccc aacactgctc aattgtcaca ataaaagtgc
   115 960
E--> 117 tatagacttg gctcccacac cacagttaaa agaaagatta gcatatgaat ttaaaggcca
   118 1020
E--> 120 ctcgttgctg caagctgcac gagaagctga tgttactcga atcaaaaaac atctctctct
   121 1080
E--> 123 ggaaatggtg aatttcaagc atcctcaaac acatgaaaca gcantgcatt gtgctgctgc
   124 1140
E--> 126 atctccatat cccaaaagaa agcaaatatg tgaactgttg ctaagaaaag gagcaamcat
   127 1200
E--> 129 caatgaaaag actaaagaat tcttgactcc tctgcacgtg gcatctgaga aagctcataa
   130 1260
E--> 132 tgatrttgtt gaagtagtgg tgaaacatga agcaaaggtt aatgctctgg ataatcttgg
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        133 1320
E--> 135 tcagacttct ctacacagag ctgcatattg tggtcatcta caaacctgcc gcctactcct
        136 1380
E--> 138 gagctatggg tgtgatccta acattatatc ccttcagggc tttactgctt tacagatggg
        139 1440
E--> 141 aaatgaaaat gtacagcaac tcctccaaga gggtatctca ttaggtaatt cagaggcaga
        142 1500
E--> 144 cagacaattg ctggaagctg caaaggctgg agatgtcgaa actgtaaaaa aactgtgtac
        145 1560
E--> 147 tgttcagagt gtcaactgca gagacattga agggcgtcag tctacaccac ttcattttgc
        148 1620
E--> 150 agctgggtat aacagagtgt ccgtggtgga atatctgcta cagcatggag ctgatgtgca
        151 1680
E--> 153 tgctaaagat aaagrrgscc ttgtaccttt gcacaatgca tgttcttatg gacattatga
        154 1740
E--> 156 agttgcagaa cttcttgtta aacatggagc agtagttaat gtagctgatt tatggaaatt
        157 1800
E--> 159 tacacctta catgaagcag cagcaaaagg aaaatatgaa atttgcaaac ttctgctcca
        160 1860
E--> 162 gcatggtgca gaccctacaa aaaaaaacag ggatggaaat actcctttgg atcttgttaa
        163 1920
E--> 165 agatggagat acagatattc aagatctgct taggggagat gcagctttgc tagatgctgc
        166 1980
E--> 168 caagaagagt tgtttagcca gagtgaagaa gttgtcttct cctgataatg taaattgccg
        169 2040
E--> 171 cgatacccaa ggcagacatt caacaccttt acatttagca gctggttata ataatttaga
        172 2100
E--> 174 agttgcagag tatttgttac aacacggagc tgatgtgaat gcccaagaca aaggaggact
        175 2160
E--> 177 tattcctttta cataatgcag catcttacgg gcatgtagat gtagcagctc tactaataaa
        178 2220
E--> 180 gtataatgca tgtgtcaatg ccacggacaa atgggctttc acacctttgc acgaagcagc
        181 2280
E--> 183 ccaaaaggga cgaacacagc tttgtgcttt gktgctagcc catggagctg acccgactct
        184 2340
E--> 186 taaaaatcag gaaggacaaa caccttttaga tttagtttca gcggatgatg tcagcgctct
        187 2400
E--> 189 tctgacagca gccatgcccc catctgctct gccctcttgt tacaagcctc aagtgctcaa
        190 2460
E--> 192 tggtgtgaga agcccaggag ccactgcaga tgctctctct tcaggtccat ctagcccatc
        193 2520
E--> 195 aagcctttct gcagccagca gtcttgacaa cttatctggg agttttttcag aactgtcttc
        196 2580
E--> 198 agtagttagt tcaagtggaa cagagggtgc ttccagtttg gagaaaaagg aggttccagg
        199 2640
E--> 201 agtagatttt agcataactc aattcgtaag gnatcttgga cttgagcacc taatggatat
        202 2700
E--> 204 atttgagaga gaacagatca ctttggatgt attagttgag atggggcaca aggagctgaa
        205 2760
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E--> 207 ggagattgga atcaatgctt atggacatag gcacaaacta attaaaggag tcgagagact
     208 2820
E--> 210 tatctccgga caacaaggtc ttaacccata tttaactttg aacacctctg gtagtggaac
     211 2880
E--> 213 aattcttata gatctgtctc ctgatgataa agagtttcag tctgtggagg aagagatgca
     214 2940
E--> 216 aagtacagtt cgagagcaca gagatggagg tcatgcaggt ggaatcttca acagatacaa
     217 3000
E--> 219 tattctcaag attcagaagg tttgtaacaa gaaactatgg gaaagataca ctcaccggag
     220 3060
E--> 222 aaaagaagtt tctgaagaaa accacaacca tgccaatgaa cgaatgctat ttcatgggtc
     223 3120
E--> 225 tccttttgtg aatgcaatta tccacaaagg ctttgatgaa aggcatgcgt acataggtgg
     226 3180
E--> 228 tatgtttgga gctggcattt attttgctga aaactcttcc aaaagcaatc aatatgtata
     229 3240
E--> 231 tggaattgga ggaggtactg ggtgtccagt tcacaaagac agatcttgtt acatttgcca
     232 3300
E--> 234 caggcagctg ctcttttgcc gggtaacctt gggaaagtct ttcctgcagt tcagtgcaat
     235 3360
E--> 237 gaaaatggca cattctcctc caggtcatca ctcagtcact ggtaggccca gtgtaaatgg
     238 3420
E--> 240 cctagcatta gctgaatatg ttatttacag aggagaacag gcttatcctg agtatttaat
     241 3480
E--> 243 tacttaccag attatgaggc ctgaaggtat ggtcgatgga taaatagtta ttttaagaaa
     244 3540
E--> 246 ctaattccac tgaacctaaa atcatcaaag cagcagtggc ctctacgttt tactcctttg
     247 3600
E--> 249 ctgaaaaaaa atcatcttgc ccacaggcct gtggcaaaag gataaaaatg tgaacgaagt
     250 3660
E--> 252 ttaacattct gacttgataa agctttaata atgtacagtg ttttctaaat atttcctgtt
     253 3720
E--> 255 ttttcagcac tttaacagat gccattccag gttaaactgg gttgtctgta ctaaattata
     256 3780
E--> 258 aacagagtta acttgaacct tttatatgtt atgcattgat tctaacaaac tgtaatgccc
     259 3840
E--> 261 tcaacagaac taattttact aatacaatac tgtgttcttt aaaacacagc atttacactg
     262 3900
E--> 264 aatacaattt catttgtaaa actgtaaata agagcttttg tactagccca gtatttattt
     265 3960
E--> 267 acattgcttt gtaatataaa tctgttttag aactgcagcg gtttacaaaa ttttttcata
     268 4020
E--> 270 tgtattgttc atctatactt gcatcttaca tcgtcatgat tgagtgatct ttacatttga
     271 4080
E--> 273 ttccagaggc tatgttcagt tgttagttgg gaaagattga gttatcagat ttaatttgcc
     274 4140
E--> 276 gatgggagcc tttatctgtc attagaaatc tttctcattt aagaacttat gaatatgctg
     277 4200
E--> 279 aagatttaat ttgtgatacc tttgtatgta tgagacacat tccaaagaac tctaactatg
```

```
          280 4260
E--> 282 ataggtcctg attactaaag aagcttcttt actggcctca atttctagct ttcatgttgg
          283 4320
E--> 285 aaaattttct gcagtccttc tgtgaaaatt agagcaaagt gctcctgttt tttagagaaa
          286 4380
E--> 288 ctaaatcttg ctgttgaaca attattgtgt tcttttcatg gaacataagt aggatgttac
          289 4440
E--> 291 atttccaggg tgggaagggt aatcctaaat catttcccaa tctattctaa ttaccttaaa
          292 4500
E--> 294 tctaaagggg aa
          295 4512
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          301 <213> ORGANISM: Artificial Sequence
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          304 <223> OTHER INFORMATION: PCR Primers
          306 <220> FEATURE:
          307 <221> NAME/KEY: CDS
          308 <222> LOCATION: (1)..(3498)
          309 <223> OTHER INFORMATION:
          312 <220> FEATURE:
          313 <221> NAME/KEY: misc_feature
          314 <222> LOCATION: (1102)..(1102)
          315 <223> OTHER INFORMATION: N is any nucleic acid
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          320 <222> LOCATION: (2650)..(2650)
          321 <223> OTHER INFORMATION: N is any nucleic acid
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          326 48
          327 Met Ser Gly Arg Arg Cys Ala Gly Gly Gly Ala Ala Cys Ala Ser Ala
          328 1               5                   10                  15
E--> 330 gcg gcc gag gcc gtg gag ccg gcc gcc cga gag ctg ttc gag gcg tgc
          331 96
          332 Ala Ala Glu Ala Val Glu Pro Ala Ala Arg Glu Leu Phe Glu Ala Cys
          333             20                  25                  30
E--> 335 cgc aac ggg gac gtg gaa cga gtc aag agg ctg gtg acg cct gag aag
          336 144
          337 Arg Asn Gly Asp Val Glu Arg Val Lys Arg Leu Val Thr Pro Glu Lys
          338         35                  40                  45
E--> 340 gtg aac agc cgc gac acg gcg ggc agg aaa tcc acc ccg ctg cac ctc
          341 192
          342 Val Asn Ser Arg Asp Thr Ala Gly Arg Lys Ser Thr Pro Leu His Leu
          343     50                  55                  60
E--> 345 gcc gca ggt ttt ggg cgg aaa gac gta gtt gaa tat ttg ctt cag aat
          346 240
          347 Ala Ala Gly Phe Gly Arg Lys Asp Val Val Glu Tyr Leu Leu Gln Asn
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Input Set : **A:\EP.txt**
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      348 65                      70                   75                   80
E--> 350 ggt gca aat gtc caa gca cgt gat gat ggg ggc ctt att cct ctt cat
      351 288
      352 Gly Ala Asn Val Gln Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His
      353                     85                   90                   95
E--> 355 aat gca tgc tct ttt ggt cat gct gaa gta gtc aat ctc ctt ttg cga
      356 336
      357 Asn Ala Cys Ser Phe Gly His Ala Glu Val Val Asn Leu Leu Leu Arg
      358         100                 105                 110
E--> 360 cat ggt gca gac ccc aat gct cga gat aat tgg aat tat act cct ctc
      361 384
      362 His Gly Ala Asp Pro Asn Ala Arg Asp Asn Trp Asn Tyr Thr Pro Leu
      363         115                 120                 125
E--> 365 cat gaa gct gca att aaa gga aag att gat gtt tgc att gtg ctg tta
      366 432
      367 His Glu Ala Ala Ile Lys Gly Lys Ile Asp Val Cys Ile Val Leu Leu
      368     130                 135                 140
E--> 370 cag cat gga gct gag cca acc atc cga aat aca gat gga agg aca gca
      371 480
      372 Gln His Gly Ala Glu Pro Thr Ile Arg Asn Thr Asp Gly Arg Thr Ala
      373 145                 150                 155                 160
E--> 375 ttg gat tta gca gat cca tct gcc aaa gca gtg ctt act ggt gaa tat
      376 528
      377 Leu Asp Leu Ala Asp Pro Ser Ala Lys Ala Val Leu Thr Gly Glu Tyr
      378                 165                 170                 175
E--> 380 aag aaa gat gaa ctc tta gaa agt gcc agg agt ggc aat gaa gaa aaa
      381 576
      382 Lys Lys Asp Glu Leu Leu Glu Ser Ala Arg Ser Gly Asn Glu Glu Lys
      383                 180                 185                 190
E--> 385 atg atg gct cta ctc aca cca tta aat gtc aac tgc cac gca agt gat
      386 624
      387 Met Met Ala Leu Leu Thr Pro Leu Asn Val Asn Cys His Ala Ser Asp
      388         195                 200                 205
E--> 390 ggc aga aag tca act cca tta cat ttg gca gca gga tat aac aga gta
      391 672
      392 Gly Arg Lys Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn Arg Val
      393     210                 215                 220
E--> 395 aag att gta cag ctg tta ctg caa cat gga gct gat gtc cat gct aaa
      396 720
      397 Lys Ile Val Gln Leu Leu Leu Gln His Gly Ala Asp Val His Ala Lys
      398 225                 230                 235                 240
E--> 400 gat aaa ggt gat ctg gta cca tta cac aat gcc tgt tct tat ggt cat
      401 768
      402 Asp Lys Gly Asp Leu Val Pro Leu His Asn Ala Cys Ser Tyr Gly His
      403                 245                 250                 255
E--> 405 tat gaa gta act gaa ctt ttg gtc aag cat ggt gcc tgt gta aat gca
      406 816
      407 Tyr Glu Val Thr Glu Leu Leu Val Lys His Gly Ala Cys Val Asn Ala
      408         260                 265                 270
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      411 864
      412 Met Asp Leu Trp Gln Phe Thr Pro Leu His Glu Ala Ala Ser Lys Asn
      413         275             280             285
  E--> 415 agg gtt gaa gta tgt tct ctt ctc tta agt tat ggt gca gac cca aca
      416 912
      417 Arg Val Glu Val Cys Ser Leu Leu Leu Ser Tyr Gly Ala Asp Pro Thr
      418         290             295             300
  E--> 420 ctg ctc aat tgt cac aat aaa agt gct ata gac ttg gct ccc aca cca
      421 960
      422 Leu Leu Asn Cys His Asn Lys Ser Ala Ile Asp Leu Ala Pro Thr Pro
      423 305             310             315             320
  E--> 425 cag tta aaa gaa aga tta gca tat gaa ttt aaa ggc cac tcg ttg ctg
      426 1008
      427 Gln Leu Lys Glu Arg Leu Ala Tyr Glu Phe Lys Gly His Ser Leu Leu
      428             325             330             335
  E--> 430 caa gct gca cga gaa gct gat gtt act cga atc aaa aaa cat ctc tct
      431 1056
      432 Gln Ala Ala Arg Glu Ala Asp Val Thr Arg Ile Lys Lys His Leu Ser
      433             340             345             350
  E--> 435 ctg gaa atg gtg aat ttc aag cat cct caa aca cat gaa aca gca ntg
      436 1104
  W--> 437 Leu Glu Met Val Asn Phe Lys His Pro Gln Thr His Glu Thr Ala Xaa
      438             355             360             365
  E--> 440 cat tgt gct gct gca tct cca tat ccc aaa aga aag caa ata tgt gaa
      441 1152
      442 His Cys Ala Ala Ala Ser Pro Tyr Pro Lys Arg Lys Gln Ile Cys Glu
      443         370             375             380
  E--> 445 ctg ttg cta aga aaa gga gca amc atc aat gaa aag act aaa gaa ttc
      446 1200
  W--> 447 Leu Leu Leu Arg Lys Gly Ala Xaa Ile Asn Glu Lys Thr Lys Glu Phe
      448 385             390             395             400
  E--> 450 ttg act cct ctg cac gtg gca tct gag aaa gct cat aat gat rtt gtt
      451 1248
  W--> 452 Leu Thr Pro Leu His Val Ala Ser Glu Lys Ala His Asn Asp Xaa Val
      453             405             410             415
  E--> 455 gaa gta gtg gtg aaa cat gaa gca aag gtt aat gct ctg gat aat ctt
      456 1296
      457 Glu Val Val Val Lys His Glu Ala Lys Val Asn Ala Leu Asp Asn Leu
      458             420             425             430
  E--> 460 ggt cag act tct cta cac aga gct gca tat tgt ggt cat cta caa acc
      461 1344
      462 Gly Gln Thr Ser Leu His Arg Ala Ala Tyr Cys Gly His Leu Gln Thr
      463             435             440             445
  E--> 465 tgc cgc cta ctc ctg agc tat ggg tgt gat cct aac att ata tcc ctt
      466 1392
      467 Cys Arg Leu Leu Leu Ser Tyr Gly Cys Asp Pro Asn Ile Ile Ser Leu
      468         450             455             460
  E--> 470 cag ggc ttt act gct tta cag atg gga aat gaa aat gta cag caa ctc
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Input Set : A:\EP.txt
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      472 Gln Gly Phe Thr Ala Leu Gln Met Gly Asn Glu Asn Val Gln Gln Leu
      473 465             470             475             480
E--> 475 ctc caa gag ggt atc tca tta ggt aat tca gag gca gac aga caa ttg
      476 1488
      477 Leu Gln Glu Gly Ile Ser Leu Gly Asn Ser Glu Ala Asp Arg Gln Leu
      478             485             490             495
E--> 480 ctg gaa gct gca aag gct gga gat gtc gaa act gta aaa aaa ctg tgt
      481 1536
      482 Leu Glu Ala Ala Lys Ala Gly Asp Val Glu Thr Val Lys Lys Leu Cys
      483             500             505             510
E--> 485 act gtt cag agt gtc aac tgc aga gac att gaa ggg cgt cag tct aca
      486 1584
      487 Thr Val Gln Ser Val Asn Cys Arg Asp Ile Glu Gly Arg Gln Ser Thr
      488             515             520             525
E--> 490 cca ctt cat ttt gca gct ggg tat aac aga gtg tcc gtg gtg gaa tat
      491 1632
      492 Pro Leu His Phe Ala Ala Gly Tyr Asn Arg Val Ser Val Val Glu Tyr
      493      530             535             540
E--> 495 ctg cta cag cat gga gct gat gtg cat gct aaa gat aaa grr gsc ctt
      496 1680
W--> 497 Leu Leu Gln His Gly Ala Asp Val His Ala Lys Asp Lys Xaa Xaa Leu
      498 545             550             555             560
E--> 500 gta cct ttg cac aat gca tgt tct tat gga cat tat gaa gtt gca gaa
      501 1728
      502 Val Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu Val Ala Glu
      503             565             570             575
E--> 505 ctt ctt gtt aaa cat gga gca gta gtt aat gta gct gat tta tgg aaa
      506 1776
      507 Leu Leu Val Lys His Gly Ala Val Val Asn Val Ala Asp Leu Trp Lys
      508             580             585             590
E--> 510 ttt aca cct tta cat gaa gca gca gca aaa gga aaa tat gaa att tgc
      511 1824
      512 Phe Thr Pro Leu His Glu Ala Ala Ala Lys Gly Lys Tyr Glu Ile Cys
      513             595             600             605
E--> 515 aaa ctt ctg ctc cag cat ggt gca gac cct aca aaa aaa aac agg gat
      516 1872
      517 Lys Leu Leu Leu Gln His Gly Ala Asp Pro Thr Lys Lys Asn Arg Asp
      518      610             615             620
E--> 520 gga aat act cct ttg gat ctt gtt aaa gat gga gat aca gat att caa
      521 1920
      522 Gly Asn Thr Pro Leu Asp Leu Val Lys Asp Gly Asp Thr Asp Ile Gln
      523 625             630             635             640
E--> 525 gat ctg ctt agg gga gat gca gct ttg cta gat gct gcc aag aag agt
      526 1968
      527 Asp Leu Leu Arg Gly Asp Ala Ala Leu Leu Asp Ala Ala Lys Lys Ser
      528             645             650             655
E--> 530 tgt tta gcc aga gtg aag aag ttg tct tct cct gat aat gta aat tgc
      531 2016
```

```
        532 Cys Leu Ala Arg Val Lys Lys Leu Ser Ser Pro Asp Asn Val Asn Cys
        533             660             665             670
E--> 535 cgc gat acc caa ggc aga cat tca aca cct tta cat tta gca gct ggt
        536 2064
        537 Arg Asp Thr Gln Gly Arg His Ser Thr Pro Leu His Leu Ala Ala Gly
        538             675             680             685
E--> 540 tat aat aat tta gaa gtt gca gag tat ttg tta caa cac gga gct gat
        541 2112
        542 Tyr Asn Asn Leu Glu Val Ala Glu Tyr Leu Leu Gln His Gly Ala Asp
        543             690             695             700
E--> 545 gtg aat gcc caa gac aaa gga gga ctt att cct tta cat aat gca gca
        546 2160
        547 Val Asn Ala Gln Asp Lys Gly Gly Leu Ile Pro Leu His Asn Ala Ala
        548 705             710             715             720
E--> 550 tct tac ggg cat gta gat gta gca gct cta cta ata aag tat aat gca
        551 2208
        552 Ser Tyr Gly His Val Asp Val Ala Ala Leu Leu Ile Lys Tyr Asn Ala
        553             725             730             735
E--> 555 tgt gtc aat gcc acg gac aaa tgg gct ttc aca cct ttg cac gaa gca
        556 2256
        557 Cys Val Asn Ala Thr Asp Lys Trp Ala Phe Thr Pro Leu His Glu Ala
        558             740             745             750
E--> 560 gcc caa aag gga cga aca cag ctt tgt gct ttg ktg cta gcc cat gga
        561 2304
W--> 562 Ala Gln Lys Gly Arg Thr Gln Leu Cys Ala Leu Xaa Leu Ala His Gly
        563             755             760             765
E--> 565 gct gac ccg act ctt aaa aat cag gaa gga caa aca cct tta gat tta
        566 2352
        567 Ala Asp Pro Thr Leu Lys Asn Gln Glu Gly Gln Thr Pro Leu Asp Leu
        568     770             775             780
E--> 570 gtt tca gcg gat gat gtc agc gct ctt ctg aca gca gcc atg ccc cca
        571 2400
        572 Val Ser Ala Asp Asp Val Ser Ala Leu Leu Thr Ala Ala Met Pro Pro
        573 785             790             795             800
E--> 575 tct gct ctg ccc tct tgt tac aag cct caa gtg ctc aat ggt gtg aga
        576 2448
        577 Ser Ala Leu Pro Ser Cys Tyr Lys Pro Gln Val Leu Asn Gly Val Arg
        578             805             810             815
E--> 580 agc cca gga gcc act gca gat gct ctc tct tca ggt cca tct agc cca
        581 2496
        582 Ser Pro Gly Ala Thr Ala Asp Ala Leu Ser Ser Gly Pro Ser Ser Pro
        583             820             825             830
E--> 585 tca agc ctt tct gca gcc agc agt ctt gac aac tta tct ggg agt ttt
        586 2544
        587 Ser Ser Leu Ser Ala Ala Ser Ser Leu Asp Asn Leu Ser Gly Ser Phe
        588             835             840             845
E--> 590 tca gaa ctg tct tca gta gtt agt tca agt gga aca gag ggt gct tcc
        591 2592
        592 Ser Glu Leu Ser Ser Val Val Ser Ser Ser Gly Thr Glu Gly Ala Ser
```

RAW SEQUENCE LISTING   DATE: 10/24/2002
PATENT APPLICATION: US/10/019,980A   TIME: 16:07:59

Input Set : A:\EP.txt
Output Set: N:\CRF4\10242002\J019980A.raw

```
        593        850                   855                   860
E--> 595 agt ttg gag aaa aag gag gtt cca gga gta gat ttt agc ata act caa
     596 2640
     597 Ser Leu Glu Lys Lys Glu Val Pro Gly Val Asp Phe Ser Ile Thr Gln
     598 865                   870             875                   880
E--> 600 ttc gta agg nat ctt gga ctt gag cac cta atg gat ata ttt gag aga
     601 2688
W--> 602 Phe Val Arg Xaa Leu Gly Leu Glu His Leu Met Asp Ile Phe Glu Arg
     603                   885                   890                   895
E--> 605 gaa cag atc act ttg gat gta tta gtt gag atg ggg cac aag gag ctg
     606 2736
     607 Glu Gln Ile Thr Leu Asp Val Leu Val Glu Met Gly His Lys Glu Leu
     608             900                   905                   910
E--> 610 aag gag att gga atc aat gct tat gga cat agg cac aaa cta att aaa
     611 2784
     612 Lys Glu Ile Gly Ile Asn Ala Tyr Gly His Arg His Lys Leu Ile Lys
     613             915                   920                   925
E--> 615 gga gtc gag aga ctt atc tcc gga caa caa ggt ctt aac cca tat tta
     616 2832
     617 Gly Val Glu Arg Leu Ile Ser Gly Gln Gln Gly Leu Asn Pro Tyr Leu
     618             930                   935                   940
E--> 620 act ttg aac acc tct ggt agt gga aca att ctt ata gat ctg tct cct
     621 2880
     622 Thr Leu Asn Thr Ser Gly Ser Gly Thr Ile Leu Ile Asp Leu Ser Pro
     623 945                   950                   955                   960
E--> 625 gat gat aaa gag ttt cag tct gtg gag gaa gag atg caa agt aca gtt
     626 2928
     627 Asp Asp Lys Glu Phe Gln Ser Val Glu Glu Glu Met Gln Ser Thr Val
     628                   965                   970                   975
E--> 630 cga gag cac aga gat gga ggt cat gca ggt gga atc ttc aac aga tac
     631 2976
     632 Arg Glu His Arg Asp Gly Gly His Ala Gly Gly Ile Phe Asn Arg Tyr
     633             980                   985                   990
E--> 635 aat att ctc aag att cag aag gtt  tgt aac aag aaa cta  tgg gaa aga
     636 3024
     637 Asn Ile Leu Lys Ile Gln Lys Val  Cys Asn Lys Lys Leu  Trp Glu Arg
     638             995                   1000                   1005
E--> 640 tac act  cac cgg aga aaa gaa  gtt tct gaa gaa aac  cac aac cat
     641 3069
     642 Tyr Thr  His Arg Arg Lys Glu  Val Ser Glu Glu Asn  His Asn His
     643       1010                   1015                   1020
E--> 645 gcc aat  gaa cga atg cta ttt  cat ggg tct cct ttt  gtg aat gca
     646 3114
     647 Ala Asn  Glu Arg Met Leu Phe  His Gly Ser Pro Phe  Val Asn Ala
     648       1025                   1030                   1035
E--> 650 att atc  cac aaa ggc ttt gat  gaa agg cat gcg tac  ata ggt ggt
     651 3159
     652 Ile Ile  His Lys Gly Phe Asp  Glu Arg His Ala Tyr  Ile Gly Gly
     653       1040                   1045                   1050
```

RAW SEQUENCE LISTING   DATE: 10/24/2002
PATENT APPLICATION: US/10/019,980A   TIME: 16:07:59

Input Set : A:\EP.txt
Output Set: N:\CRF4\10242002\J019980A.raw

```
E--> 655 atg ttt  gga gct ggc att tat  ttt gct gaa aac tct  tcc aaa agc
     656 3204
     657 Met Phe  Gly Ala Gly Ile Tyr  Phe Ala Glu Asn Ser  Ser Lys Ser
     658     1055                1060               1065
E--> 660 aat caa  tat gta tat gga att  gga gga ggt act ggg  tgt cca gtt
     661 3249
     662 Asn Gln  Tyr Val Tyr Gly Ile  Gly Gly Gly Thr Gly  Cys Pro Val
     663     1070                1075               1080
E--> 665 cac aaa  gac aga tct tgt tac  att tgc cac agg cag  ctg ctc ttt
     666 3294
     667 His Lys  Asp Arg Ser Cys Tyr  Ile Cys His Arg Gln  Leu Leu Phe
     668     1085                1090               1095
E--> 670 tgc cgg  gta acc ttg gga aag  tct ttc ctg cag ttc  agt gca atg
     671 3339
     672 Cys Arg  Val Thr Leu Gly Lys  Ser Phe Leu Gln Phe  Ser Ala Met
     673     1100                1105               1110
E--> 675 aaa atg  gca cat tct cct cca  ggt cat cac tca gtc  act ggt agg
     676 3384
     677 Lys Met  Ala His Ser Pro Pro  Gly His His Ser Val  Thr Gly Arg
     678     1115                1120               1125
E--> 680 ccc agt  gta aat ggc cta gca  tta gct gaa tat gtt  att tac aga
     681 3429
     682 Pro Ser  Val Asn Gly Leu Ala  Leu Ala Glu Tyr Val  Ile Tyr Arg
     683     1130                1135               1140
E--> 685 gga gaa  cag gct tat cct gag  tat tta att act tac  cag att atg
     686 3474
     687 Gly Glu  Gln Ala Tyr Pro Glu  Tyr Leu Ile Thr Tyr  Gln Ile Met
     688     1145                1150               1155
E--> 690 agg cct  gaa ggt atg gtc gat  gga
     691 3498
     692 Arg Pro  Glu Gly Met Val Asp  Gly
     693     1160                1165
     1047 <210> SEQ ID NO: 6
     1048 <211> LENGTH: 19
     1049 <212> TYPE: DNA
     1050 <213> ORGANISM: Artificial Sequence
     1052 <220> FEATURE:
     1053 <223> OTHER INFORMATION: PCR Primers
     1055 <400> SEQUENCE: 6
E--> 1056 cccgagagct gttcgaggc
     1057 19
     1060 <210> SEQ ID NO: 7
     1061 <211> LENGTH: 23
     1062 <212> TYPE: DNA
     1063 <213> ORGANISM: Artificial Sequence
     1065 <220> FEATURE:
     1066 <223> OTHER INFORMATION: PCR Primers
     1068 <400> SEQUENCE: 7
E--> 1069 caatctttac tctgttatat cct
```

RAW SEQUENCE LISTING   DATE: 10/24/2002
PATENT APPLICATION: US/10/019,980A   TIME: 16:07:59

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\10242002\J019980A.raw**

```
       1070 23
       1073 <210> SEQ ID NO: 8
       1074 <211> LENGTH: 41
       1075 <212> TYPE: DNA
       1076 <213> ORGANISM: Artificial Sequence
       1078 <220> FEATURE:
       1079 <223> OTHER INFORMATION: PCR Primers
       1081 <400> SEQUENCE: 8
E--> 1082 aagcggccgc attatggaaa ggatcatgtc gggtcgccgc t
       1083 41
       1086 <210> SEQ ID NO: 9
       1087 <211> LENGTH: 25
       1088 <212> TYPE: DNA
       1089 <213> ORGANISM: Artificial Sequence
       1091 <220> FEATURE:
       1092 <223> OTHER INFORMATION: PCR Primers
       1094 <400> SEQUENCE: 9
E--> 1095 aaggatccac cataccttca ggcct
       1096 25
       1099 <210> SEQ ID NO: 10
       1100 <211> LENGTH: 39
       1101 <212> TYPE: DNA
       1102 <213> ORGANISM: Artificial Sequence
       1104 <220> FEATURE:
       1105 <223> OTHER INFORMATION: PCR Primers
       1107 <400> SEQUENCE: 10
E--> 1108 aaaagcttta tggaaaggat catgtcgggt cgccgctgc
       1109 39
```

VERIFICATION SUMMARY   DATE: 10/24/2002
PATENT APPLICATION: US/10/019,980A   TIME: 16:08:00

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\10242002\J019980A.raw**

```
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:34 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:1
L:47 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:2
L:69 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:3
M:254 Repeated in SeqNo=3
L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:1080
L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2640
L:318 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:309
L:325 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:4
M:254 Repeated in SeqNo=4
L:435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:1056
L:437 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:1104
L:447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:1200
L:452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:1248
L:497 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:1680
L:562 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:2304
L:600 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:2640
L:602 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:2688
L:839 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:352
L:847 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:384
L:851 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:400
L:887 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:544
L:939 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:752
L:971 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:880
L:1056 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:6
L:1069 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:7
L:1082 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:41 SEQ:8
L:1095 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:9
L:1108 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:10
```